

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/170,042

DATE: 03/17/2000  
TIME: 11:30:50

INPUT SET: S35072.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: HASTINGS, GREGG,  
PATRICK J. DILLON

(ii) TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
(B) STREET: 9410 KEY WEST AVENUE  
(C) CITY: ROCKVILLE  
(D) STATE: MD  
(E) COUNTRY: USA  
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/170,042  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/799,173  
(B) FILING DATE: 11-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BROOKES, ANDERS A.  
(B) REGISTRATION NUMBER: 36,373  
(C) REFERENCE/DOCKET NUMBER: PF226

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504  
(B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

ENTERED  
RECEIVED  
MAR 22 2000  
TC 1000 MAIL ROOM

# RAW SEQUENCE LISTING PATENT APPLICATION US/09/170,042

 DATE: 03/17/2000  
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47 (A) LENGTH: 1105 base pairs  
 48 (B) TYPE: nucleic acid  
 49 (C) STRANDEDNESS: single  
 50 (D) TOPOLOGY: linear

51 (ii) MOLECULE TYPE: DNA (genomic)

52 (ix) FEATURE:

53 (A) NAME/KEY: CDS  
 54 (B) LOCATION: 19..1011

55 (ix) FEATURE:

56 (A) NAME/KEY: mat\_peptide  
 57 (B) LOCATION: 19..963

58 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

|    |   |     |
|----|---|-----|
| 51 | CGCTGCTCCT GCCGGGTG ATG GAA AAC CCC AGC CCG GCC GCC GCC CTG GGC | 51  |
| 66 | Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly                     |     |
| 67 | 1 5 10  |     |
| 68 |   |     |
| 69 | AAG GCC CTC TGC GCT CTC CTC CTG GCC ACT CTC GGC GCC GCC GGC CAG | 99  |
| 70 | Lys Ala Leu Cys Ala Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln |     |
| 71 | 15 20 25  |     |
| 72 |   |     |
| 73 | CCT CTT GGG GGA GAG TCC ATC TGT TCC GCC AGA GCC CTG GCC AAA TAC | 147 |
| 74 | Pro Leu Gly Gly Glu Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr |     |
| 75 | 30 35 40  |     |
| 76 |   |     |
| 77 | AGC ATC ACC TTC ACG GGC AAG TGG AGC CAG ACG GCC TTC CCC AAG CAG | 195 |
| 78 | Ser Ile Thr Phe Thr Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln |     |
| 79 | 45 50 55  |     |
| 80 |   |     |
| 81 | TAC CCC CTG TTC CGC CCC CCT GCC CAG TGG TCT TCG CTG CTG GGC GCC | 243 |
| 82 | Tyr Pro Leu Phe Arg Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala |     |
| 83 | 60 65 70 75   |     |
| 84 |   |     |
| 85 | GCG CAT AGC TCC GAC TAC AGC ATG TGG AGG AAG AAC CAG TAC GTC AGT | 291 |
| 86 | Ala His Ser Ser Asp Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser |     |
| 87 | 80 85 90  |     |
| 88 |   |     |
| 89 | AAC GGG CTG CGC GAC TTT GCG GAG CGC GGC GAG GCC TGG GCG CTG ATG | 339 |
| 90 | Asn Gly Leu Arg Asp Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met |     |
| 91 | 95 100 105  |     |
| 92 |   |     |
| 93 | AAG GAG ATC GAG GCG GCG GGG GAG GCG CTG CAG AGC GTG CAC GCG GTG | 387 |
| 94 | Lys Glu Ile Glu Ala Ala Gly Glu Ala Leu Gln Ser Val His Ala Val |     |
| 95 | 110 115 120   |     |
| 96 |   |     |
| 97 | TTT TCG GCG CCC GCC GTC CCC AGC GGC ACC GGG CAG ACG TCG GCG GAG | 435 |
| 98 | Phe Ser Ala Pro Ala Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu |     |
| 99 |   |     |

 RECEIVED  
 MAR 22 2003  
 TC 1600 MAIL ROOM

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|     |  |     |     |      |
|-----|--|-----|-----|------|
| 100 | 125  | 130 | 135 |      |
| 101 |  |     |     | 483  |
| 102 | CTG GAG GTG CAG CGC AGG CAC TCG CTG GTC TCG TTT GTG GTG CGC ATC    |     |     |      |
| 103 | Leu Glu Val Gln Arg Arg His Ser Leu Val Ser Phe Val Val Arg Ile    |     |     |      |
| 104 | 140  | 145 | 150 | 155  |
| 105 |  |     |     | 531  |
| 106 | GTG CCC AGC CCC GAC TGG TTC GTG GGC GTG GAC AGC CTG GAC CTG TGC    |     |     |      |
| 107 | Val Pro Ser Pro Asp Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys    |     |     |      |
| 108 |  | 160 | 165 | 170  |
| 109 |  |     |     | 579  |
| 110 | GAC GGG GAC CGT TGG CGG GAA CAG GCG GCG CTG GAC CTG TAC CCC TAC    |     |     |      |
| 111 | Asp Gly Asp Arg Trp Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr    |     |     |      |
| 112 |  | 175 | 180 | 185  |
| 113 |  |     |     | 627  |
| 114 | GAC GCC GGG ACG GAC AGC GGC TTC ACC TTC TCC TCC CCC AAC TTC GCC    |     |     |      |
| 115 | Asp Ala Gly Thr Asp Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala    |     |     |      |
| 116 |  | 190 | 195 | 200  |
| 117 |  |     |     | 675  |
| 118 | ACC ATC CCG CAG GAC ACG GTG ACC GAG ATA ACG TCC TCC TCT CCC AGC    |     |     |      |
| 119 | Thr Ile Pro Gln Asp Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser    |     |     |      |
| 120 |  | 205 | 210 | 215  |
| 121 |  |     |     | 723  |
| 122 | CAC CCG GCC AAC TCC TTC TAC TAC CCG CGG CTG AAG GCC CTG CCT CCC    |     |     |      |
| 123 | His Pro Ala Asn Ser Phe Tyr Tyr Pro Arg Leu Lys Ala Leu Pro Pro    |     |     |      |
| 124 |  | 220 | 225 | 230  |
| 125 |  |     |     | 235  |
| 126 | ATC GCC AGG GTG ACA CTG GTG CGG CTG CGA CAG AGC CCC AGG GCC TTC    |     |     | 771  |
| 127 | Ile Ala Arg Val Thr Leu Val Arg Leu Arg Gln Ser Pro Arg Ala Phe    |     |     |      |
| 128 |  | 240 | 245 | 250  |
| 129 |  |     |     | 819  |
| 130 | ATC CCT CCC GCC CCA GTC CTG CCC AGC AGG GAC AAT GAG ATT GTA GAC    |     |     |      |
| 131 | Ile Pro Pro Ala Pro Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp    |     |     |      |
| 132 |  | 255 | 260 | 265  |
| 133 |  |     |     | 867  |
| 134 | AGC GCC TCA GTT CCA GAA ACG CCG CTG GAC TGC GAG GTC TCC CTG TGG    |     |     |      |
| 135 | Ser Ala Ser Val Pro Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp    |     |     |      |
| 136 |  | 270 | 275 | 280  |
| 137 |  |     |     | 915  |
| 138 | TCG TCC TGG GGA CTG TGC GGA GGC CAC TGT GGG AGG CTC GGG ACC AAG    |     |     |      |
| 139 | Ser Ser Trp Gly Leu Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys    |     |     |      |
| 140 |  | 285 | 290 | 295  |
| 141 |  |     |     | 963  |
| 142 | AGC AGG ACT CGC TAC GTC CGG GTC CAG CCC GCC AAC AAC GGG AGC CCC    |     |     |      |
| 143 | Ser Arg Thr Arg Tyr Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro    |     |     |      |
| 144 |  | 300 | 305 | 310  |
| 145 |  |     |     | 315  |
| 146 | TGC CCC GAG CTC GAA GAA GAG GCT GAG TGC GTC CCT GAT AAC TGC GTC    |     |     | 1011 |
| 147 | Cys Pro Glu Leu Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val    |     |     |      |
| 148 |  | 320 | 325 | 330  |
| 149 |  |     |     | 1071 |
| 150 | TAAGACCAGA GCGCCGACGC CCCTGGGGGCC CCGCGAGGCC ATGGGGTGTC GGGGGCTCCT |     |     |      |
| 151 |  |     |     | 1105 |
| 152 | GTGCAGGCTC ATGCTGCAGG CGGCCGAGGG CACA                              |     |     |      |

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155 (2) INFORMATION FOR SEQ ID NO:2:

156

157 (i) SEQUENCE CHARACTERISTICS:

158 (A) LENGTH: 331 amino acids

159 (B) TYPE: amino acid

160 (D) TOPOLOGY: linear

161

162 (ii) MOLECULE TYPE: protein

163

164 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

165

166 Met Glu Asn Pro Ser Pro Ala Ala Ala Leu Gly Lys Ala Leu Cys Ala  
167 1 5 10 15168 Leu Leu Leu Ala Thr Leu Gly Ala Ala Gly Gln Pro Leu Gly Gly Glu  
169 20 25 30  
170171 Ser Ile Cys Ser Ala Arg Ala Leu Ala Lys Tyr Ser Ile Thr Phe Thr  
172 35 40 45  
173174 Gly Lys Trp Ser Gln Thr Ala Phe Pro Lys Gln Tyr Pro Leu Phe Arg  
175 50 55 60  
176177 Pro Pro Ala Gln Trp Ser Ser Leu Leu Gly Ala Ala His Ser Ser Asp  
178 65 70 75 80  
179180 Tyr Ser Met Trp Arg Lys Asn Gln Tyr Val Ser Asn Gly Leu Arg Asp  
181 85 90 95  
182183 Phe Ala Glu Arg Gly Glu Ala Trp Ala Leu Met Lys Glu Ile Glu Ala  
184 100 105 110  
185186 Ala Gly Glu Ala Leu Gln Ser Val His Ala Val Phe Ser Ala Pro Ala  
187 115 120 125  
188189 Val Pro Ser Gly Thr Gly Gln Thr Ser Ala Glu Leu Glu Val Gln Arg  
190 130 135 140  
191192 Arg His Ser Leu Val Ser Phe Val Val Arg Ile Val Pro Ser Pro Asp  
193 145 150 155 160  
194195 Trp Phe Val Gly Val Asp Ser Leu Asp Leu Cys Asp Gly Asp Arg Trp  
196 165 170 175  
197198 Arg Glu Gln Ala Ala Leu Asp Leu Tyr Pro Tyr Asp Ala Gly Thr Asp  
199 180 185 190  
200201 Ser Gly Phe Thr Phe Ser Ser Pro Asn Phe Ala Thr Ile Pro Gln Asp  
202 195 200 205  
203204 Thr Val Thr Glu Ile Thr Ser Ser Ser Pro Ser His Pro Ala Asn Ser  
205

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|     | 210   | 215                         | 220                     |
|-----|---|-----------------------------|-------------------------|
| 206 |   |                             |                         |
| 207 |   |                             |                         |
| 208 | Phe Tyr Tyr Pro Arg   | Leu Lys Ala Leu Pro         | Pro Ile Ala Arg Val Thr |
| 209 | 225   | 230                         | 235 240                 |
| 210 |   |                             |                         |
| 211 | Leu Val Arg Leu Arg Gln Ser Pro Arg                             | Ala Phe Ile Pro Pro Ala Pro |                         |
| 212 |   | 245                         | 250 255                 |
| 213 |   |                             |                         |
| 214 | Val Leu Pro Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser Val Pro |                             |                         |
| 215 |   | 260                         | 265 270                 |
| 216 |   |                             |                         |
| 217 | Glu Thr Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser Trp Gly Leu |                             |                         |
| 218 |   | 275                         | 280 285                 |
| 219 |   |                             |                         |
| 220 | Cys Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser Arg Thr Arg Tyr |                             |                         |
| 221 |   | 290                         | 295 300                 |
| 222 |   |                             |                         |
| 223 | Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro Cys Pro Glu Leu Glu |                             |                         |
| 224 |   | 305                         | 310 315 320             |
| 225 |   |                             |                         |
| 226 | Glu Glu Ala Glu Cys Val Pro Asp Asn Cys Val                     |                             |                         |
| 227 |   | 325                         | 330                     |

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCCATACGGG ATCCCCAGCC TCTTGGGGGA GAGTCC

36

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

PAGE: 1

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/170,042**

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*INPUT SET: S35072.raw*

Line

Error

Original Text